```
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2001, 13:35:37; search time 62.8 Seconds

(without alignments)

268.371 Million cell updates/sec

Title: US-09-668-482-2

Sequence: 1 MGLYTLMYFELCTIVLPVLL......GPTIXPVDNLPTKFTSYVRN 492

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Total number of hits satisfying chosen parameters: 93435

Post-processing: Minimum Match 0%

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_39:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		crip	P79739 brachvdanio		7 mus m	~		023051 arabidopsis							P51538 rattus norv		P29980 anabaena sp	Q42600 arabidopsis	Q64481 mus musculu	P10614 saccharomyc	P79401 sus scrofa	sns	P05184 homo sapien		P14579 oryctolagus			m	m	_		046051 drosophila	0	_	Q64654 rattus norv
\$ SUMMARIES	Query	D	CP26_BRARE	CP26_HUMAN	CP26_MOUSE	C901_ARATH	m	C883_ARATH	C881_MAIZE	C136_MYCTU	CP3R_ONCMY	CP36_RABIT	CPC9_HUMAN	CPCA_HUMAN	CP39_RAT	C4D8_DROME	CPXN_ANASP	CP84_ARATH	CP3G_MOUSE	CP51_YEAST	CP3T_PIG	CP51_PIG	CP33_HUMAN	CP3S_BOVIN	CP45_RABIT	C131_DROME	CP48_RAT	CPCB_RAT	CP3C_CANFA	CP3E_CAVPO	CP34_HUMAN	C4DE_DROME	CP51_HUMAN	C7B1_THLAR	CP51_RAT
		Match Length DB				472 1																											503 1		
		Match	100.0	6.79	~	21.6	α	^	4	4	ന	m	ന	ന	ന	$^{\circ}$	$^{\circ}$	$^{\circ}$	α	\sim	$^{\circ}$	$^{\circ}$	12.7	Α.	N I	ά,	α;	ά,	Ċ.	ς.	ď	ς.		12.4	7
		Score	2563	1741	1734	552.5	481	450	375	363	350.5	343.5	339.5	339.5	333	331	330.5	330.5	329	328.5	326	326	324.5	324.5	324	323.5	323.5	322.5	322.5	322.5	320	320	318	317.5	317
	Result	No.	П	2	m	4	w.	9	7	œ ·	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	2.4	25	26	7.7	28	29	30	31	32	33

062671 canis famil 081970 glycine max P1481 oryctolagus Q6406 cavia porce P05183 rattus norv 09w011 drosophila 027599 drosophila 022307 lotus japon P33561 homo sapien P20815 homo sapien P20815 homo sapien Q6459 mus musculu 029496 ovis aries	15 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4) (Zebra danio). ; Craniata; Vertebrata; Buteleostomi; Teleostei; Buteleostei; Ostariophysi; asborinae; Danio.	-Jones B., Bonasoro J., vyich M.; all-trans-retinoic	acid 4. hydroxylase."; J. Biol. Chem. 271:2922-29927(1996). J. Biol. Chem. 271:2922-29927(1996). -!- FUNCTION: PLAYE A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON FETINOIDS. INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS STEREOISOMER 9-CIS-RA. CAPABLE OF 4-HYDROXYLATION; HYDROXYLATION RESPONSIBLE FOR GENERALION OF SEVERAL HYDROXYLATED FORMS OF RA,		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMEL; U68234; AAC60045.1; - ZFIN; ZDB-GENE-990415.44; cyp26. InterPro; IPR001128; - PAGN; PR0067; p450; 1. PRINTS; PR00385; P450. Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum. BINDING 438 438 438 BINDING 492 AA, 56281 MW; FP471435B2P30599 CRC64;); DB 1; Length 492; 2.9e-140; les 0; Indels 0; Gaps 0;
CANFA SOYBN RABIT CAVPO CAVPO DROME DROME LOTJA HUMAN MOUSE	ALIGNMENT	upda on ur ETINC D 4-F	a dar ata; tei; ae; I	ckett Petko d-ind). ETINC RETINO OF 4-	BOUNI A). CHRON	It information in formation in formation in the state of	1. rane; BY SI	ore 2563; ed. No. 2. Mismatches
CPZ6_CANFA C719_SOYBN CP47_RABIT CP47_RABIT CP32_RAT C4DZ_DROME C7DB_LOTOR C7DB_LOTOR CPC7_HUMAN CP31_MMAN CP31_MMAN CP31_MUMAN	ALIG PPT.	uence otati -) (R C ACI	(Zebr Crani eleos borin	36; ., Be G., c aci	(1996 IN R RANS- ABLE OF S	O-RA. RANE- DS (R CYTO	ight. f Bio stitu ons a not reeme	26. P450; ;; Memb HEME (
		ted) seq:ann 4	sh) ita; i; T ƙas	9399 tz K Ones	9927 ROLE LLL-T CAP	4-0X MEMB	copyrical copyri	CYP2 CYP2 axe;	
ааааааааааа 		rea ast ast 1.1	afi rda ygi ae;	d≂8 Bae , J	EY EY G B	S S S S	s c itu tic tric sti sti men ens	1; 4; HRO 9en	0.0
84 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	י וט פרוא פודי. י רוט פרוא	8 (Rel. 37, Cl 8 (Rel. 37, La 8 (Rel. 37, La P450 26 (EC) (P450RAI) (B	orio (Zebrafish) (Zebra darazoa: Chordata; Craniata; I. Neopterygil; Teleostel; Cyprinidae; Rasborinae; Es;	PubMe -D., F.J.	:2992 S A K LUDIN -CIS-	CATIONES	try instructions formation formation formation formation formation for the following f	0045.1; 415-44; Cyl 8; 0; 1. 450. CYTOCHROME_ nooxygenase 1um. 56281 MW;	100.0%; ilarity 100.0%; Conservative 0
155555333333	E S	1. 1. 2.6 5.0 R	io zoa Ne Cyp	Z; Y. of	ase 271 271 LAY INC R 9	E SE	en iss oin ofi is	AC6 9990 9990 112 112 945 MO icu	ity ser
		(Re (Re (Re 2450	rer Meta Jii;	M M 3470 Guo Cllwo	oxyl	WG 4 MLAR NN:	PROT Bib 1 Bib 1 - Pro 1 th Muir	1, A. 2NE- 2NE- 2NE- 300 37;] 385; 386; 186; 186; 197;]	Llar
34 315.5 37 315.3 37 314.5 38 314.5 39 314.5 41 311.5 42 311.5 44 311.5 45 311.5	RESULT 1 CP26_BRARE IN CP26 RRARE	P79739; 15-DEC-1998 (Rel. 37, 15-DEC-1998 (Rel. 37, 15-DEC-1998 (Rel. 37, CYTCCHROME P450 26 (B CXTCCHROME) (P450RAI)	Crrzb. Brachydanio rerio Bukaryota; Metazo Actinopterygil; N Cypriniformes; Cy NCBI_TAXID=7955;	[1] SEQUENCE FRC MEDLINE=9705 White J.A., Hsu K.E., Di	acid 4-hydro J. Biol. Che -!- FUNCTION RETINOII STEREOIS	INCLUDIN -!- SUBCELLU -!- INDUCTIC -!- SIMILARI	This SWISS-I between the the Europear use by nor modified and entities req	EMBL; U66234; AAC6004 ZFIN; ZDB-GENR-990415; InterPro; IFR01128; Pfan; PR00667; P450; PRINTS; PR00385; P450 PROSITE; P800086; CYFO Oxidoreductase; Moncos Endoplasmic reticulum BINDING 438 438 SEQUENCE 492 AA; 58	Query Match Best Local Similarity Matches 492; Conser
	RESU CP26		00000 00000000000000000000000000000000	RN RP RA RA	##S8888	88888	388888888	CC DR DR MWW MW MW MW MW MW MW MW MW MW MW MW MW	Qu Be Ma

```
||:||||||| :|| :
477 SPIVYPVDNLPARFIHF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
          NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \overline{Q}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98380037; PubMed-9716180; Sonneveld E., van den Brink C.E., van der Leede B.M., Schulkes R.K., Petkovich M., van der Burg B., van der Saag P.T.; "Human retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific for all-trans-RA and can be induced through RA receptors in human breast and colon carcinoma cells.";
                                                                                       120
                                                                                                         121 GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYĮPVIQQEVKSAIQEWLQKDSCVLVYPEM 180
                                                                                                                                                                                            KKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRARNFI 240
                                                                                                                                                                                                                                                                                241 HSKIEBNIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHET 300
                                                                                                                                                                                                                                                                                                                                                             301 TASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDGSKFNYIPFGGGSRMCVGKEFAKVLAKIFLVELTQHCHWILSNGPPTMKTGPTIXPVD 480
      09
                            MEDLINE-99045433; PubMed=9826557;
Trofimova-Griffin M.E., Juchau M.R.;
"Expression of cytochrome P450RAI (CYP26) in human fetal hepatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97373542; PubMed-9228017; White J.A., Beckett-Jones B., Guo Y.-D., Dilworth F.J., Bonasoro J., Jones G., Petkovich M.; "cDNA cloning of human retinoic acid-metabolizing enzyme (hP450RAL) identifies a novel family of cytochromes P450."; J. Biol. Chem. 272:18538-18541(1997).
                                                                                 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL
MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 RINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 26 (EC 1.14...) (RETINGIC ACID-METABOLIZING
CYPCCHROME) (REJORAL) (RETINGIC ACID 4-HYDROXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9:629-637(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carcinoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPTKFTSYVRN 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell Growth Differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CP26_HUMAN
043174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE
                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CP26_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÿ
                                   QQ
                                                                                 ð
                                                                                                                      g
                                                                                                                                                           ΩŽ
                                                                                                                                                                                                                                                   δŽ
                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΩŸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ů,
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
cephalic tissues.",
Biochem. Biophys. Res. Commun. 252:487-491(1998).

1- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS STEREDISOMER 9-CIS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-HYDROXYLATION RESPONSIBLE FOR GENERALTHON OF SEVERAL HYDROXYLATED FORMS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.

1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.

1- TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIYER, HERRT, PITUITARY GLAND, ADRENAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.

1- INDUCTION: BY RETINOIC ACIDS (RA).

1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC----VLV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILQRRKFIRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 YPEMKKLMFRIAMRILLGFEPEQIKTD---EQELVEAFEEMIKNLFSLPIDVPFSGLYRG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRARNFIHSKIEENIRKKIQD-DDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 ERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EABGB84B24B2EAB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1741; DB 1;
Pred. No. 3.8e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF005418; AAB88881.1; -.
MIM; 602239; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 AA; 56162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%;
68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 GPTIYPVDNLPTKFTSY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 68.2
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001128; -. Pfam; PF00067; p450; 1. PRINTS; PR00385; P450.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
STROUNCE FROM N.A.
STRAIN-CV. COLUMBLE.
MEDLINE-96200769; PubMed=8612270;
MEDLINE-96200769; PubMed=8612270;
MEDLINE-96200769; PubMed=8612270;
Altmann T., Redei G.P., Nagy F., Scheli J., Koncz C.;
Altmann T., Redei G.P., Nagy F., Scheli J., Koncz C.;
Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450, Controlling cell elongation and de-etiolation in Arabidopsis.";
Cell 85:171-182(1996).
Cell 85:171-182(1996).
                                      235 RARNFIHSKIEENIRKKIQD-DDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATEL 293
                                                                                                                                                                                                                                                                                                                                                                                                     294 LFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                               354 CVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 REMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC----VLV 176
                                                                                                                                                                                                                                                                                                                                  238 KARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTEL 297
                                                                                                                                 177 YPEMKKIMFRIAMRILLGFEPEQI--KTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEME (BY SIMILARITY).
41A73F46D64E343F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase;
BINDING 418 418 HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X87367; CAA60793.1; -. EMBL; X87368; CAA60794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:||||||| :|| :
478 PTVYPVDNLPARFTYF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 PTIYPVDNLPTKFTSY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001128; -. Pfam; PF00067; p450; 2. PROSITE; PS00086; CXTOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C901 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C901_ARATH
ID C901_A
   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOUR DE RESERVANTE DE PROPERTIES DE PROPERTI
                                                               g
                                                                                                                              δž
                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                     δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98113212; PubMed-9442090; Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G., Metager D., Chambon P., Petkovich M.; "Mouse P450RAI (CYP26) expression and retinoic acid inducible retinoic acid metabolism in F9 calls are regulated by retinoic acid receptor gamma and retinoid X receptor alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON RETINOIDS, INCLUDING ALL-FRANDER PERINOIC ACID METABOLISM. ACTS ON RETINOIDS, INCLUDING ALL-FRANDER PERINOIC ACID (FAS) AND ITS STEREOISOMER 9-CS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-HYDROXYLATION AND 18-HYDROXYLATION OF SEVERAL HYDROXYLATED FOWNS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.

1- SUBCELLUJAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULDM.

1- INDUCTION: BY RETINOIC ACIDS (RA).

1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMIMIRRVDPNCRSPLPPGTMGLPFIGETLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujil H., Sator T., Kaneko S., Gotoh O., Fujil-Kuriyama Y., Osawa K., Kato S., Hamada H.; Kaneko S., Gotoh O., Fujil-Kuriyama Y., Osawa K., "Metabolic inactivation of retinoic acid by a novel P450 differentially expressed in developing mouse embryos."; EMBO J. 16:4163-4173(1997).
                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CTTOCHROME P450 26 (EC 1.14...) (RETINOIC ACID-METABOLIZING
CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE),
CYP26A1 OR CYP26 OR P450RA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.7%; Score 1734; DB 1; Length 497; 67.7%; Pred. No. 9.7e-93; Live 61; Mismatches 89; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 442 HEME (POTENTIAL).
497 AA; 56177 MW; 33B07D7C29134471 CRC64;
                                                               497 AA.
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97392446; PubMed=9250660;
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y12657; CAA73206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 07.70
nes 336; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1096359; Cyp26.
InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                        CP26_MOUSE
055127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                            CP26_MOUSE
```

q

ă

qq

ΩŸ

13;

Query Match

Matches

δŻ g δ, 음

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUMBIA;
Osborne B.I., Vysotskaia V.S., Federspiel N.A.,
Osborne B.I., Vysotskaia V.S., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422
                                                                                                                                                                                                                                                                                                                                                                                     80 KTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKKA 139
                                                                                                                                                                                                                                                                                                                                                                                                              341 ATIVNGVLRKTTQDMEINGYIIPKGWRIYVYTRELNYDPRLYPDPYSFNPWRWMDKSLEH 400
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                    LFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQRRKFLRMKRQKYGCIY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 EIQHDMLGYLANBERTRFK------LTDDE-----MIDLITILYSGYETYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 MMAVKYLHDHPKVLEELRKEHMAIREKKK-----PEDPIDYNDYRSMRFTRAVILETSRL
                                                                                                                                                                                                                                                                                                                                             16 IFCTALLRWNQVKYNQKN-----LPPGTMGWPLFGETTEFLKLGPSFMKNQRARYGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 IMRAFS----RDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRAR----NFIHSKIEE-NIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIQDD-----DNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 NPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDIHDVADVFPNKEEFQPERFMSKGLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 TSLVMFLGLNTEVVQKVREE---VQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRI
                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                 Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 GSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toriumí M., Tu G., Oji O., Araujo R., Chung E., Dewar K., Ecker J.R., Marziali A., Oefrer P., Davis R.W., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. - Submitted (SEP-1997) to THE CYTOCHROWE P450 FAMILY.
                                                                                                                                                                                                                                                            192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | : ||||:| | ||| : || 401 ONSF--LVFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMK
                                                                                                                           HEME (BY SIMILARITY).
D2B21AAAB7B14E94 CRC64;
                                                                                                                                                                                                          ; Score 481; DB 1;
; Pred. No. 5.9e-21;
90; Mismatches 192;
                                      Pfan, PP00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Moncoxygenase; Heme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 88A3 (EC 1.14...).
CYFP88A3 OR YUP8H12.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                53706 MW;
                                                                                                                                                                                                            Query Match 18.8%;
Best Local Similarity 28.4%;
Matches 133; Conservative 90.
U54770; AAB17070.1;
Pro; IPR001128; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. COLUMBIA;
Theologis A., Osborne
                                                                                                                                                  464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C883_ARATH
                                                                                                                                                    SEQUENCE
                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
C883_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŽ
  δŽ
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                       Q_{\overline{A}}
                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato).
Eukaryota; Viridiolantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                    306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461
                                                                                                                                                                                                               66 RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH 125
                                                                                                                                                                                                                                                                                                                                             192 LLGFEP----EQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR-GLRARNFIHSKIEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 SLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 LAVKFLTETPLALAQLKEE-HEKIR-AMKSDSYSLEWSDYKSMPFTQCVVNETLRVANII 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 GGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQSNSVTTGPSN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 NYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPIMKTGPTIYPVDNLPTKF 486
                                          Gaps
                                                                                     73
                                                                                                            SEQUENCE FROM N.A.
STRAIN-GY. GCR758;
MEDLINE-9.666705; PubMed=8672892;
Bishop G.J., Harrison K., Jones J.J.G.D.;
"The tomato Dwarf gene isolated by heterologous transposon tagging encodes the first member of a new cytochrome P450 family.";
                                                                                                                                                                                                                                                                                                                                                                        247 NIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 VVMKR-REEEEEGAERKKDMLAALL----AADDGFSDEEIVDFLVALLVAGYETTSTIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 PGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRF
                                                                                   ----LQRRKFLRMKRQ
                                                                                                                                                                                                                                                            134 KNKKKAIMRAFSRDAL -- EHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRI
                                        37;
  Length 472;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYPSE OR D. CYPSE OR D. CYPSE OR D. CYPSE OR D. CYPSE OR D.
  DB 1;
                                          205;
                                                                                   19 LLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-
                      4.8e-25
                                        98; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA
  Score 552.5;
Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
  21.6%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Cell 8:959-969(1996)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 TSYVR 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 PIFVK 466
                                        145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CP85_LYCES
```

LYCES

qq Qγ 임 Qy a QY 셤

Dp ΟŽ QQ ŏ

셤 ŏ

δ

between

```
21 PC
466 HE
57906 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
 Gibberellin biosynthesis.";
                                                                                                                                                                                     EMBL; U32579; AAC49067.1; -.
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                   InterPro; IPR001128;
                                                                                                                                                                                                                                                                466 4
519 AA;
                                                                                                                                                                                                                                                                                                                              Local Similarity
les 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C136_MYCTU
P95099;
                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C136_MYCTU
  g
                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \Omega
                                                                                                                                                                                                                            10;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@disb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388
                                                                                                                                                                                                                                                                                                                                                                                216
                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 LLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 NVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 SDTCRRVLTDDDAF-KPGWPTSTMELIGRKSFVGISFEEHKRLRRLTAAPVNGHEALSTY 160
                                                                                                                                                                                                                                                                                                                                                       153 IPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFE 212
                                                                                                                                                                                                                                                                                                                                                                                                       213 EMIKNLFSLPIDVPFSGLYRGLRARNFIHSKIEENIRKKIQDDDNENEQKY----KDALQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 NILINVKDEDGKTLDDEEIIDVLLMYLNAGHESSGHTIMMATVFLQEHPEVLQRAKAE-QE 331
                                                                                                                                                                                                                                                                          42 RHYLPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKGIYKAHMFGNPSIIVTT 101
                                                                                                                                                                                                                                                                                                     94 ADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKKAIMRAFS-RDALEHY 152
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Winkler R.G., Helentjaris T.;
"The maize Dwarf3 gene encodes a cytochrome P450-mediated early step
                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                       217 ALNYGVRAMAVNIPGFAYHRALKARKTLVAAFQSIVTER----RNQRKQNILSNKKDMLD
                                                                                                                                                                                                                                                    41 RSPLPPGTMGLPFIGETLQLILQRR----KFLRMKRQKYG--CIYKTHLFGNPTVRVMG
                                                                                                                                                                                                                                                                                                                                                                     329 KVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGW
                                                                                                                                                                                                                            24;
                                                                                                                                                                                                   Length 490;
                                                                                                                                                                                                                            220; Indels
                                                                                                                                                               7FD8CD7A8864D298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHENME P450 88A1 (EC 1.14.-.-) (DWARF3 PROTEIN).
CYPB8A1 OR D3.
                                                                                                                        Oxidoreductase; Monooxygenase; Transmembrane; Heme-
TRANSMEM 6 26 POTENTIAL.
BINDING 439 439 HEME (BY SIMILARITY).
                                                                                                                                                                                                   17.6%; Score 450; DB 1; 27.6%; Pred. No. 3.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 AA
                                                                                                                                                                                                                           84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 KIFLVELTQHCNWILSNGPPTMKTGPTIYPVDN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIFLHHFLLKYQVKRSNPECPVMYLPHTRPTDN 482
                                                                                                  PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96004534; PubMed=7549486;
                                                               EMBL; AC000098; AAB71462.1; -.
                                                                                                                                                               56409 MW;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                         Pro; IPR001128; -.
PF00067; p450; 1.
                                                                                                                                                                490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=CV. B73;
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                              Query Match
Best Local Simil
Matches 125; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C881_MAIZE
Q43246;
                                                                             InterPro;
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
  g
                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                  ΟŽ
                                                                                                                                                                                                                                                                                                                                                                                                                          Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                       \nabla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q_{\overline{\Lambda}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                     δÿ
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                       Ö
```

```
This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AEGCKQVIMDDDAFVT-GWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGF--DALT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 HYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 --DALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 KAE-QEAIMRSIPSSQRGLTLRDFRKMEYLSQVIDETLRLVNISFVSFRQATRDVFVNGY 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 QIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 LIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWEGHSPRAGT---FLAFGLGARLCPGND 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 ADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKK---AIMRAFSRDALE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 GVDMMDRLIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 RSPLPPGTMGLPFIGETLQLILQRRK-----FLRMKRQKYG--CIYKTHLFGNPTVRVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 REEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGY
                                                                          LEAVES, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GYLPFIDRIVISSLRAWADHGGSVEFLIELRRMIFKIIVQIFLG-GADQATI--RALERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 FEEMIKNLFSLPIDVPFSGLYRG-LRARNFIHSKIEENIRKKIQDDDNENEQKYK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7AX-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PUTATIVE CYTOCHROME P450 136 (EC 1.14.-.-).
PUTATIS OR RV3059 OR MICY22D7.22C.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Plant Cell 7:1307-1317(1995).
--- PATHWAT: BARLY STPP IN GIBEBEBLLIN BIOSYNTHESIS.
--- PATHWAT: BARLY STPP IN GIBEB IN ROOTS, DEVELOPING
---- TISSUE SPECTFICITY: EXPRESSED IN ROOTS, DEVELOPING
VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEME (BY SIMILARITY).
: 0F8977A024316D95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLPTKFT 487
                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
OXIGORGALCIASE; MOTOCXYGENASE; Transmembrane; Heme.
TRANSMEM 1 2.1
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 375; DB 25.6%; Pred. No. 8e-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492
```

13;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h. Biochem. Biophys. 360:53-61(1998).
FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
NONOXYGENSARSES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
OF STRUCTURALLY UNKLAIED COMPOUNDS, INCLUDING STEROIDS, PATTY
ACIDS, AND XENOBIOTICS.
CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES, AND CARCINOGENS.
410 FQPERFMS-KGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILS--NG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   new member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OXIDIZED FLAVOPROTEIN + H(2)0.
SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERVINGE FROM N.A.
STRAINSCHASTA; TISSUE-Liver;
MEDLINE-99045386; PubMed=9826429;
Lee S.-J., Wang-Buhler J.-L., Cok I., Yu T.S., Yang Y.H.,
Lee S.-J., Wang-Buhler D.R.;
"Cloning, sequencing, and tissue expression of CYP3A27, a new rolf the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from From Portion of The CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and adult rainbow trout of the CYP3A subfamily from embryonic and the CYP3A subfamily from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEME (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Last annotation update) (EC 1.14.14.1) (CYPIIIA27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsome; Endoplasmic_reticulum.
BINDING 447 447 HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequ
15-JUL-1999 (Rel. 38, Last anno
CYTOCHROME P450 3A27 (EC 1.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U96077; AAB82422.1; -.
                                                                                                                                                                                                                                                                                            467 PPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                                                                                                                                                                                                         470 OPRWDYSAMPIPMDGMP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001128; ...
InterPro; IPR002397; ...
InterPro; IPR002401; ...
InterPro; IPR002402; ...
InterPro; IPR002403; ...
Pfam; PF00067; Pf50; I.
PRINIS; PR00359; BP450; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP450II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00465; EP450IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00385; P450.
PR00463; EP450I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CP3R_ONCMY
042563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYP3A27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
CP3R_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HERE WERE REPORTED TO THE PROPERTY OF THE PROP
                                                                                                                        δλ
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgimeier K., Gas S., Barry C.E. Ili, Terkaia F., Badcock K., Bashmeier K., Gas S., Barry C.E. Ili, Terkaia F., Davies R., Davies R., Perwn D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyk S., Oldrors S., Caperne J., Quail M.A., Majandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ALTLDIASMVEMGHEP----GTDHELVTKVNKAFTITTRAGNAVIRT--SVP---PFT-W 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCIYKTH----LFGN-----PTVRVMGADNVRQILLGEHKLVSVQ-W-----PASVRTILGS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 --LYKTKGPVVFGDSAVLPGVAALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRGLMLL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 DILSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAI-QEWLQKDSCVLVYPEMK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 DF----EEHMFHRRIMQEAFVRSRLAGYLEQMDRVVSRVVADDWVVNDARFLVYPAMK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 KLMFRIAMRILLGFEPEQIKTDEQELV------EAFEEMIKNLFSLPIDVPFSGL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 YRGLRARNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 WRGLRARELLENYFTARVKERREASGN-----DLLTVLCQTEDDDGNRFSDADIVNHM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 TELLFGGHETTASTATSIVMFIGLNTEVVQKVREEVQEKVENGMYTPGKG-LSMELLDQL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 KYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 MSLVEHMLINTKFPEKKLAEPPPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLMF---- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 VKLWEMLMIRRVDPNCRSPLPP-----GIMGLPFIGETLQLILQRRKFLRMKRQKY 75
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%; Score 363; DB 1; Length 492; 26.0%; Pred. No. 3.7e-14; Live 82; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOCHROME_P450; 1.
Pin; Oxidoreductase; Monooxygenase; Heme.
43c27 WW; BOA78FCE95622R3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : - SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                      MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 283866; CAB06263.1; -.
TubercuList; Rv3059; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00067; p450; 1.
PRINTS; PR00389; BP450.
PRINTS; PR00463; EP450.
PRINTS; PR00463; EP450I.
PRINTS; PR00465; EP450IV.
PROSITE; PS00086; CYTOCHRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001128; ...
InterPro; IPR002397; ...
InterPro; IPR002401; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002403; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 129; Conserv
                                                                                                                        FROM N.A.
                                               NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
```

OY Db Oy Db

_

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Gasge by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      EMBL; M19199; AAA314301.1; BRBL; M19199; AAA314301.1; BRBL; J05034; AAA31478.1; -...

RE EMBL, J05034; AAA31430.1; -...

RE AAA31478.1; -...

RE AAA31478.1; -...

RE AAA31478.1; -...

RE AAA31478.1; -...

RE INTERPO: IPRO02397; -...

RE INTERPO: IPRO02402; -...

RE INTERPO: IPRO02402; -...

RE INTERPO: PRO0667; P450; -...

RE RIMIS; PRO0464; EP4501.

RE RIMIS; PRO0464; EP4501.

RE RIMIS; PRO0464; EP4501.

RE RIMIS; PRO0466; CYPOCHROME P450; 1...

REAR AAA314301.

REAR AAA314301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGL-SMELLDQLKYTG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 LKTSVE-----KIKDDRLKDKQKRRVDFLQLMINSQNSKEIDSHKALDDIEVVAQSIIIL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYVNETLRLYPIAGRLERVCKKDVDINGTFIPKGTIVMMPTYALHRDPQHWTEPDEFRPE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGTMGLPFIGETLQLILQRRK----FLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQIL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 PGPTPLPFIG----TILEYRKGIWDFDIECRKKYGKMWGLFDGRQPLMVITDPDMIKTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 MRAFSRDALEHYIPVIQQE----VKSAIQEWLQKDSCVLVYPEMKKIMFRIAMRIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 LGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDV----PF-SGLYRGLR-----ARNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGVNIDSLRNPODPFVKNVRRLLKFSFFDPLLLSITLFPFLTPIFEALHISMFPKDVMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHSKIEENIRKKIQDDDNENEQKYK-DALQLLI--ENSRRSDEPFSLQAMKEAATE--LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWIL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI -> VIN (IN REF. 1).
GKPVD -> ASPST (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RD -> ES (IN REF. 1).
251D21061863ACFB CRC64;
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 VKECYSVFINRRSFGPVGFMKKAVSISEDEDW-KRVRTLLSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 343.5; DB 1; Pred. No. 4.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKPVD -/ ALL
MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
169
393
495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
   SO THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE THE TERM DEATH THE TERM DEATH THE TERM DEATH THE TERM DEATH THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q_{Y}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 YNIFTHRRNFHLNGEL-FDALSVAEDDTWRRIRSVLSPSFFTSGRLKEMFGIMKOHSSTLI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLIENSRRSDEPFSLQAMK-----EAATELLFGGHETTASTATSLVMFLGLNTEVVQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 KVREEVQEKVEMGMYTPGKG-LSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFEL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 NGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 SGMKKQADKDQTI----EVKEFFGPYSMDVVTSTAFSVDIDSLNNPSDPFVSNVKKMLKF 214
                                                                                                                                                                                                                                                                                                                                         HKLVSVQWPASVRIILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQE---VK 161
                                                                                                                                                      Gaps
                                                                                                                                                                                                               PCIMGLPFIGETLQLILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGE- 104
                                                                                                                                                                                                                                                                      40 PGPKPLPYFGTMLEYKKGFTNFDTECFQKYGRIWGIYDGRQPVLCIMDKSMIKTVLIKEC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88866352; PubMed-3349903; Dalet C., Clair P., Daujat M., Fort P., Blanchard J.-M., Maurel P.; Complete sequence of cytochrome P450 3c cDNA and presence of two manna species with 3' untranslated regions of different lengths."; DNA 7:39-46(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89380226; PubMed=2777787;
Potenza C.L., Pendurthi U.R., Strom D.K., Tukey R.H., Griffin K.J., Schwab G.E., Johnson E.F.;
"Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and transcriptional activation by rifampicin.";
J. Biol. Chem. 264:16222-16228[1989).
-!- FUNCTION: EXHIBITS PROGESTERONE 6 BETA-HYDROXYLASE ACTIVITY.
-!- CATALITY ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 SAIQEWLQKDSCVLVYPEMKKLMFRIAMRIL----LGFEPEQIKTDEQELVEAFEEMIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NLFSLPIDVPFSGLYRGLRARNFIHSKIEE----NIRKKIQDDDNENEQKYKDALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLFNPLFLLVALFPFTGPILEKMKFSFFPTAVTDFFYASLAKIKSGRDTGNSTNRVDFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYP3Ab.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION; MEMBRANE-BOUND, ENDOPLASMIC RETICULUM -!- INDUCTION; BY RIFAMPICIN.
                                                                                                                                                      37;
                                                                                         Length 518;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CP36_RABIT STANDARD; PRT; 501 AA. P11707; 029506; P01707; 029506; P01707; Created) P15-JUL-1999 (Rel. 18, Last sequence update) P15-JUL-1999 (Rel. 38, Last annotation update) CXTOCHROME P450 3A6 (EC 1.14.14.1) (CYPIIIA6) (P450-3C).
9B93AA12E617D0DF CRC64;
                                                                                         DB 1;
                                                                                      13.7%; Score 350.5; DB 25.6%; Pred. No. 2e-13;
                                                                                                                                               Mismatches
                                                                                                                                               83;
   59210 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | :::|: ||: |
| 449 GMRFALIMIKLAMVEILQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 GKEFAKULLKIFLVELTQ 457
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
   AA;
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
   518
   SEQUENCE
                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
CP36_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYP3A6
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              So
                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                         ă
                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΛ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q_{\overline{Y}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

19;

Gaps

93;

Indels

294

```
S06863; S06863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                                                                                                                                        359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Sim
hes 139;
                                                                                                                                                                                                                                                                                         Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhasker C.R., Winers J.O., Coulter S., Birkett D.J.;
Allelic and functional variability of cytochrome P4502C9.";
Pharmacogenetics 7:51-56(1997).
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOXYCBRARSES. IN LIVER MICROSOMES, THIS BRIZME IS INVOLYED IN AN
NADDH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VAREETY
OF SIRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FAITY
                                                                                30-XAY-2000 (Rel. 39, Last Sequence update)
30-XAY-2000 (Rel. 39, Last annotation update)
30-YAY-2000 (Rel. 39, Last annotation update)
30-YAY-2000 (Rel. 39, Last 14.14.1) (CYPLIC9) (P450 PB-1) (P450 MP-4)
(S-WEPHRNYTOIN 4-HYDROXIASE) (P-450MP).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDDMed-2827463; MEDLINE-88103561; PubMed-2827463; Meehan R.R., Gosden J.R., Rout D., Hastie N.D., Friedberg T., Meehan R.R., Buckland R., van Heyningen V., Fletcher J., Spurr N.K., Sweeney J., Wolf C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88096500; pubMed=3697070;
Kimura S., Pastewka J., Gelboin H.V., Gonzalez F.J.;
"CDNA and amino acid sequences of two members of the human P450IIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 108-490 FROM N.A.
SEQUENCE OF 108-490 FROM N.A.
Ged C., Umbenhauer D.R., Bellew T.M., Bork R.W., Srivastava P.K.,
Shinriki N., Lloyd R.S., Guengerich F.P.;
"Characterization of CDNAS, mRNAS, and proteins related to human
liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase."
Blochemistry 27:6929-6940(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-i- DATABASE: NAME-Cytochrome P450 Allele Nomenclature Committee;
NOTE-CYP2C9 alleles;
                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                      "Muman cytochrome P-450 PB-1: a multigene family involved in mephenytoin and steroid oxidations that maps to chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97101957; PubMed=8946475;
Stubbins M.J., Harries L.W., Smith G., Tarbit M.H., Wolf C.R.;
"Genetic analysis of the human cytochrome P450 CYP2C9 locus.";
Pharmacogenetics 6:429-438(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWW-"http://www.imm.ki.se/CYPalleles/cyp2c9.htm".
                    490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene subfamily.";
Nucleic Acids Res. 15:10053-10054(1987)
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIDIZED FLAVOPROTEIN + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 42:26-37(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97264536; PubMed=9110362;
                                                                  01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: BY RIFAMPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACIDS, AND XENOBIOTICS,
                         STANDARD;
                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Hum.
                       CPC9_HUMAN
P11712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS
```

```
I -> L (IN CYP2C9*3; RESPONSIBLE FOR THE TOLBUTAMIDE POOR METABOLIZER PHENOTYPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNQPSEFTIESLENTAVDLFGAGTETTSTILRYALLLLUKHPEVTAKVQEBIERVI---- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 YTPGKGLS--MELLDQLKYTGCVIKETLRINPPVPGGFRVALK-TFELNGYQIPKGWNVI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GRNRSPCMODRSHMPYTDAVVHEVORYIDELPTSLPHAVTCDIKFRNYLIPKGTTIL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDILSNVHGVQHKNKKK-AIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSD-EPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SLVVLVLC---LSCLILLS---LWR-----QSSGRGKLPPGPTPLPVIGNILQIGIKD 49
InterPro; IPR001128; -.
InterPro; IPR001397; -.
InterPro; IPR003401; -.
InterPro; IPR003401; -.
Pfam; PF00075; P450; 1.
PRINTS; PR00385; P4450.
PRINTS; PR00463; E24501.
PRINTS; PR00463; E24501.
PRINTS; PR00465; E24501.
PRINTS; PR00465; E24501.
PROSITE; PR00666; CXTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TIMVIFICTIVLPVLEFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL-ILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 RRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQIL--LGEHKLVSVQWPASVRTILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ISKSLINLSKVYGPVFTLYFGLKPIVVLHGYEAVKEALIDLGEEFSGRGIFPLAERANRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FGIVFSNGKKWKEIRRFSLMTLRNF-----GMGKRSIEDRVQEEARCLVEELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KKIMFRIAMRILLGFEPEQI------KIDEQ--ELVEAFEEMIK-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 LFSLPIDVPFSGLYRGLRARN--FIHSKIEENIRKKIQDDDNENEQKYKDALQLLIENSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 YSICDT-HDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEFAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> I (IN REF. 2).
C -> Y (IN REF. 1).
F -> L (IN REF. 1).
4FDFC395303A4E3E CRC64;
                                                                                                                                                                                                                                                                        reticulum; Polymorphism.
HEME (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                             R -> C (IN CYP2C9*2)
/FIId=VAR_008343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 339.5; DB 1 26.9%; Pred. No. 8.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELFLITSILQNFNLKSLVDPKNLDTTPVVNGFASVP 480
                                                                                                                                                                                                                                                                                                                                                              Y -> C.
/FTId=VAR_008344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_008345.
G -> D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_008346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
175
239
55627 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                     Endoplasmic r
435 435
144 144
                                                                                                                                                                                                                                                                                                                                                                 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
```

22;

EMBL; M21940; AAA52159.1; -.

PIR; A28530; A28530.

RESULT 12 CPCA HUMAN

TISSUE=Liver;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CP39_RAI STANDARD; PRT; 503 AA.
P51538; Q64631; Q64557;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME P450 3A9 (EC 1.14.14.1) (CYPIIIA9) (P450-OLF3) (OLFACTIVE)
                                                      ---GRNRSPCMQDRSHMPYTDAVVHEVQRCIDLLPTSLPHAVTCDIKFRNYLIPRGTTIL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 YSICDI-HDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEFAKV 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 ISLTSVLHDNKE-FPNPEMFDPHHF----LDEGDNFKKSKYFMPFSAGKRICVGEALAGM 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                            158 KTKASPCDPTFILGCAPCNVICSIIFHKRFDYKDQQFLNLMEKLNENIKILSSPWIQICN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 YTPGKGLS--MELLDQLKYTGCVIKETLRINPPVPGGFRVALK-TFELNGYQIPKGWNVI 391
                   RRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQIL--LGEHKLVSVQWPASVRTILG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                           RSD-EPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang H., Kawashina H., Strobel H.W.;
"cDNA cloning of a novel CYP3A from rat brain.";
Biochem. Biophys. Res. Commun. 221:157-162(1996).
-!- FUNCTION: THIS ISOSTWA SEEMS TO BE IMPLICATED IN OLFACTION. ACIN THE DEMETHIATION OF ERYTHROWYCIN AS WELL AS BENZPHETAMINE.
-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
                                                                                                                                                                                                                              KKIMFRIAMRILLGFEPEQI------KTDEQ--ELVEAFEEMIK------N
                                                                                                                                                                                                                                                                                                                                      218 LFSLPIDVPFSGLYRGLRARN--FIHSKIEENIRKKIQDDDNENEQKYKDALQLLIENSR
                                                                                                                                                                                                                                                                                                                                                                       218 NFSPIIDY-FPGTHNKL-LKNVAFMKSYILEKVKEHQESMDMNNPQDFIDCFLMKMEKEK
                                                                                                                              SDILSNVHGVQHKNKKK-AIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression and inducibility of cytochrome P450 3A9 (CYP3A9) and other members of the CYP3A subfamily in rat liver."; Arch. Biochem. Biophys. 337:62-68(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPITHELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: MEMBRÂNE-BOUND. ENDOPLASMIC RETICULUM.
-!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN OLFACTORY EPITHELIUM.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
MEDLINE-97144501; PubMed-8990268;
Mahnke A., Strotkamp D., Roos P.H., Hanstein W.G., Chabot G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 ELELETISILQNENIKSLVDPKNLDTTPVVNGFASVP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXIDIZED FLAVOPROTEIN + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96220175; PubMed=8660328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (3AH15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYP3A9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nef P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                              972
                                                                                                                                                                                  110
                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                    g
                                                                                                                           δy
                                                                                                                                                                            q
                                                                                                                                                                                                                                   δŽ
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.oh/announce/or send an email to license@isb-sib.oh).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AN
                                                                                                                                                                                                                                                                                                                                                                                                                Umbenhauer D.R., Martin M.V., Lloyd R.S., Guengerich F.P.; "Cloning and sequence determination of a complementary DNA related to human liver microsomal cytochrome P-450 S-mephenytoin 4-hydroxylase."; Blochemistry 26:1094-1099(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM. INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOUVERNASSE. IN LIVER MICROSOMES, THIS ENTENTE IS INVOLVED IN AN WADPH-DEPENDENT SIGNATOR TRANSPORT PRIMMAY. IT OXIDIESS A VARIETY OF STRUCTURALLY UNRELAIED COMPOUNDS, INCLUDING STEROIDS, FAITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SLVVLVLC---LSCLILLS---LWR------OSSGRCKLPPGPTPLPVIGNILOIGIKD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 6-490 FROM N.A.
MEDLINE-89063423; PubMed=3196692;
Ged C., Umbenhauer D.R., Bellew T.M., Bork R.W., Srivastava P.K.,
Shintiki N., Lioyd R.S., Genegerich F.P.;
Characterization of CDNAs, mRNAs, and proteins related to human
liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase.";
Blochemistry 27:6929-6940(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002401; -.
Pfam; PF00067; p455; 1.
PRINTS; PR00385; P450.
PRINTS; PR00465; P4501.
PROSTE: PS00066; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL-ILQ
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77;
                        01-0CT-1989 (Rel. 12, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
STOCHROME P450 2C10 (EC 1.14.14.1) (CYPITCIO) (P450 MP-8) (S-CYPOCHROME P450 2C10 (RC 1.14.14.1) (CYPITCIO) (P450 MP-8) (S-CYPOCHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Mismatches 218; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEME (BY SIMILARITY),
4FDC13A83AE494DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 339.5; DB 1.26.9%; Pred. No. 8.1e-13;
490 AA.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsome; Endoplasmic reticulum.
BINDING 435 435 HEME
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87185403; PubMed=3032244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M15331; AAA52157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M21939; AAA52158.1; -.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 6-490 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIDS, AND XENOBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001128; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A27541; A27541.
PIR; D28951; D28951.
                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 4
490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARCINOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 124020; -
```

ACTIVE

SEQUENCE BINDING

Matches

Q

δă

```
17;
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| |||| |: : : |:||| || DVEINGVEIPKGTVVMIPTFALHKDPHYWPEEFRPERFSKKNQDNINPYMYLPFGNGP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVVQKVREEVQEKVEMGMYTPGKG-LSMELLDQLKYTGCVIKETLRINPPVPGGFRVALK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 DIQKKLQDEIDAAL----PNKAHATYDTLLQMEYLDMVVNETLRLYPIAGRLERVCKT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 TFELNCYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGS 435
                                                                                                                                                                                                                                                                                                                                                                                                                     105 --HKLVSV----QWPASVRTIIGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KRIRALLSPTFTSGKLKEMFPIINQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 EVKSAIQEWLQ-----KDSCVLVYPEMKKLMFRIAMRIL----LGFEPEQIKTDEQELVE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 AFEEMIK-----NLFSLPIDVPF-SGLYRGLRARNFIHSKIE---ENIRKKIQDDDNENE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 QXYKDALQLLI -- ENSRRSDEPFSLQAMKEAATEL -- LFGGHETTASTATSLVMFLGLNT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 KQRMDFLQLMINSQNSKVKDSHKALSDVEIVAQSVIFIFAGYETTSSALSFVLYLLAIHP 325
                                                                                                                                                                                                                                                                                                                                                                                              53 YRKGFWEFDKYCHKKYGKLWGLYDGRQPVLAITDPDIIKTVLVKECYSTFINRRNFGFVG 112
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                          9 METWILLIVISLVILYLYGTHSHGIFKKLGI------PGPKPLPFLG----TILA 52
                                                                                                                                                                                                                                                                                                                       7 NVTFICTIVLPVLLFLAAVK -- - LWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQ 63
                                                                                                                                                         PRINTS; PR00464; EP45011.

PROSITE; PS00066; CYTOCHROME_P450; 1.
Oxidoreductaes; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum; Olfaction.

BINDING 442 442 HEME (BY SIMILARITY).

CONFLICT 457 457 F. -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100;
                                                                                                                                                                                                                                                                       DB 1; Length 503;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                        HEME (BY SIMILARITY).
F -> V (IN REF. 2).
9BHB13E690675EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       64 RRK----FLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGE-
                                                                                                                                                                                                                                                                      13.0%; Score 333; DB 1; L 23.5%; Pred. No. 2e-12;
tive 95; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME P450 4DB (EC 1.14.-.-) (CYPIVDB). CYP4DB OR CG4321.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 RMCVGKEFAKVLLKIFLVELTQH 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:| || ::|: |:
RNCIGMRFALMNMKVALFRVLQN 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequ
01-0CT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                     57811 MW;
                                                                                   EMBL; U60085; AAB03662.1; -. EMBL; U46118; AAC52582.1; -.
                                                                                                                                                                                                                                                                                                Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ILKKAISISEDEEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                            Interpro; IPR001128; -.
Interpro; IPR002402; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                     503 AA;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4D8_DROME (09VS79; Q24127;
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
C4D8_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q_{Y}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΫ
     a
                                                                                                                                                                                                                                                                                                                                                                     ă
                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OY
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΩŽ
                                                                                                                                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                      \Omega
```

```
PRESTYORE NEEDERSON, NATHOROGAL TREADMENT, BREADPORE; INSECUDING, MASSIVER, MASSIVER,
```

```
baena sp. strain PCC 7120 nifD element.";
Bacteriol. 172:6981-6990(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6, 2001, 13:39:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52525 MW;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U38537; AAC82967.1; -. PIR; C37842; C37842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.39
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November
Job time: 242 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrogen fixation.
BINDING 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
         Anabaena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
             ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 KGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKIFEL-----NGYQIPKGWNVIY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 SICDIHDVADVFPNKEEFQPERFMSKGLEDGSR---FNYIPFGGGSRMCVGKEFAKVLLK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Developmental rearrangement of cyanobacterial nif genes: nucleotide sequence, open reading frames, and cytochrome P-450 homology of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 KWRQTQLIRTMQEFTIKVIEKRRQALEDQQSKLMDTADEDVGSKRRMALLDVLLMSTVDG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 Q---KYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVS-----VQWPASVRTILGS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 EYVLKFGHLQRVWIFNRLLIMSGDABLNEQLLSSQEHLVKHPVYKVLGQW-----LGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 DILSNYHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQK--DSCVLVYPEM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : : | | : : | : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : : | : : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    18 VLLFLAAVKL----WEMLMIRRVDPNCRSPLPPGIMGLPFIGE-TLQLILQRRKFLRMKR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 CAAALDIIAETAMGTKIYAQANESTPYAEAVNECTALLSWRFMSVYLQVELLFTLTHPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNL-----FSLPIDVPFSGLYRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 RAR--NFIHS-----KIEENIRKKIODD------DNENEOKYKDALOLLIENSRRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 EPFSLQAMKEAATELLEGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPG
                                                                                                                                                                                                                                                                                                                                               (99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91072249; PubMed=2123860;
Lammers P.J., McLaughlin S., Papin S., Trujillo-Provencio C.,
Ryncarz A.J. II;
                                                                                                                                                                                                                                                                                                 12.9%; Score 331; DB 1; Length 505; 26.4%; Pred. No. 2.6e-12; tive 82; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                  Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
Endoplasmic reticulum;
BINDTNG AFT
                                                                                                                                                                                       A -> E (IN REF. 2).
R -> C (IN REF. 2).
7BAA5271ED46093F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 37, Last annotation update)
PROBABLE CYTOCHROME P450 110 (EC 1.14.-.-) (ORF3).
                                                                                                                                                                     HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                    InterPro, IPR001128; ... PR0067; P450; PPAn; PR00067; P450; I. PRNTS; PR00385; P450; PR0SITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                          57819 MW;
                  FlyBase; FBgn0015033; Cyp4d8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                          333
435
                                                                                                                                                                         451
                                                                                                                                                                                            333 3
435 4
505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 MMLAKIVR 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 IFLVELTQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              059131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPXN_ANASP
P29980; Q59
                                                                                                                                                                                                                                                                                                                                                   129;
                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP110.
                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
CPXN_ANASP
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩŸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                      ă
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 IYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKI 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 MASIYLIHYREDLYPUPQQFRPERFIER---QYSPSEYIPFGGGSRRCLGIALALIEIKL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 ENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGF-RVALKTFELNGYQIPKGWNV 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 QELDRLGANFNPMEIAQLPYLTAVSQETLRMYPVLPTLFPRITKSSINIAGYQLEPDTTL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 SRFDVGRGNTLAEPLIGRTSLMLMDGDRHRRERKLLMPPFHGERLQAYAQQICLIINQIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 QEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEP----EQIK---TDEQELVEA-FEEMIK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 PGIMGLPFIGETLQLILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PNPISVPSWWQLINWIADPIGFQKKYSKKYGNIFSWQLAGIGSFVILGEPQALQEIFTQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 KLVSV-QWPASVRTILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 NLFSLPID----VPFSGLYRGLRA-RNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AARDENGQAMIDEELKDELLILFAGHETIATTIAWAFY-----QILKNV--NVQEKLQ
Lammers P.J., Trujillo-Provencio C., Sanchez C., Carillo M.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY INVOLVED IN ALKANE/FATIY ACID HYDROXXLASE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; 1.
PROSITE: P500086; CYTCOHROWE P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEME (BY SIMILARITY).
67C62908C94C569B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 330.5; DB 1; 25.3%; Pred. No. 2.5e-12; tive 88; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 FLVELTQHCNWILSNGPP--TMKTGPTIYP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : : | : | : | 4.06 VIATVLSNYQLALAEDKPVNVQRRGFTLAP 435
```

14;